



SEQUENCE LISTING

<110> Nippon Institute for Biological Science

<120> novel plasmid vector

<130> PCTF0001-0

<140> 09/762,568

<141> 2001-02-06

<150> JP, Japanese Patent

<151> 1999-06-04

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed PCR primer including 3' region of U3 and VspI restriction enzyme site to multiply RSV LTR.

<400> 1

ggcattaaatg tagtcttatg caataactcct g

31

<210> 2

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed PCR primer including 5' non coding region of p19 gene, HincII, EcoRV and BglII restriction enzyme site to multiply RSV LTR and down stream region of LTR.

<400> 2

gttaaacgata tcagatctgc ttgatccacc gggcgaccag

40

<210> 3

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed PCR primer including 5' region of RSV integrase gene and BamHI restriction enzyme site to multiply RSV integrase gene.

<400> 3
ttggatccat gcccttgaga gaggctaaag atcttc 36

<210> 4
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed PCR primer including 3' region of RSV
integrase gene, polyA signal to multiply RSV
integrase gene.

<400> 4
tttattttaa ctctcggttgg cagcaagggt gtc 33

<210> 5
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed PCR primer including 5' region of U5 and
VspI restriction enzyme site to multiply RSV LTR.

<400> 5
ggcattaaatg aagccttctg cttcattca 29

<210> 6
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed PCR primer including 3' region of RSV
integrase gene, polyA signal, nuclear localization
signal of SV40 large T antigen to multiply RSV
integrase gene.

<400> 6
tttattttaa accttcctct tcttcttagg actctcggttgg gcagcaagggt t 51

<210> 7
<211> 858
<212> DNA
<213> Rous sarcoma virus

<220>
<221> TATA_signal
<222> (84)...(90)

<221> polyA_signal
<222> (107)...(112)

<221> TATA_signal
<222> (431)...(437)

<221> polyA_signal
 <222> (454)...(459)
 <223> A part of circular form of RSV DNA, tandem repeat
 LTRs and adjacent non coding region.

<400> 7
 acgatcgtgc cttatttagga aggcaacaga cgggtctaac acggattgga cgaaccactg 60
 aattccgcat tgcggagata ttgtatttaa gtgcctagct cgataacaata aaccccattt 120
 taccattcac cacattggg tgcacctggg ttgatggctg gaccgttcat tccctgacga 180
 ctacgacac atgcatgaag cagaaggctt cattaatgtt gtcttatgca atactcctgt 240
 agtcttgaa catgcttatg taacgatgag ttagcaacat gccttacaag gagagaaaag 300
 gcaccgtgca cgacgattgg tggaaagtaag gtggatgtat cgttaggtacg atcgtgcctt 360
 attaggaagg caacagacgg gtctaaacacg gattggacga accactgaat tccgcatttc 420
 ggagatattt tatttaagtgt cctagctgca tacaataaac gccatttac cattcaccac 480
 attgggtgtc acctgggttg atggctggac cgttatttcc ctgacgacta cgagcacatg 540
 catgaagcag aaggcttcat ttggtgaccgc cgacgtgatc gttagggat agtggtcggc 600
 cacagacggc gtggcgatcc tgccttcattc cgtctcgctt attcggggag cggacgatga 660
 ccctagtaga gggggctgctg gcttaggagg gcagaagctg agtggcgctg gagggagctc 720
 tactgcaggg agcccagata ccctaccgag aactcagaga gtcgttggaa gacggaaaga 780
 aagcccacg actgagcggt ccaccccagg cgtgatttcc gttgctctgc gtgaccctgg 840
 tcgcccggtg gatcaagc 858

<210> 8
 <211> 972
 <212> DNA
 <213> Rous sarcoma virus

<220>
 <221> CDS
 <222> (1)...(972)
 <223> precursor integrase or p36 protein

<221> CDS
 <222> (1)...(858)
 <223> mature integrase or p32 protein

<400> 8
 ccc ttg aga gag gct aaa gat ctt cat acc gct ctc cat att gga ccc 48
 Pro Leu Arg Glu Ala Lys Asp Leu His Thr Ala Leu His Ile Gly Pro
 1 5 10 15

cgc gcg cta tcc aaa gcg tgt aat ata tct atg cag cag gct agg gag 96
 Arg Ala Leu Ser Lys Ala Cys Asn Ile Ser Met Gln Gln Ala Arg Glu
 20 25 30

gtt gtt cag acc tgc ccg cat tgt aat tca gcc cct gcg ttg gag gcc 144
 Val Val Gln Thr Cys Pro His Cys Asn Ser Ala Pro Ala Leu Glu Ala
 35 40 45

gga gta aac cct agg ggt ttg gga ccc cta cag ata tgg cag aca gac 192
 Gly Val Asn Pro Arg Gly Leu Gly Pro Leu Gln Ile Trp Gln Thr Asp
 50 55 60

ttt acg ctt gag cct aga atg gcc ccc cgt tcc tgg ctc gct gtt act 240
 Phe Thr Leu Glu Pro Arg Met Ala Pro Arg Ser Trp Leu Ala Val Thr
 65 70 75 80

gtg gac acc gcc tca tca gcg ata gtc gta act cag cat ggc cgt gtc		288
Val Asp Thr Ala Ser Ser Ala Ile Val Val Thr Gln His Gly Arg Val		
85	90	95
aca tcg gtt gct gta caa cat cat tgg gcc acg gct atc gcc gtt ttg		336
Thr Ser Val Ala Val Gln His His Trp Ala Thr Ala Ile Ala Val Leu		
100	105	110
gga aga cca aag gcc ata aaa aca gat aac ggg tcc tgc ttc acg tct		384
Gly Arg Pro Lys Ala Ile Lys Thr Asp Asn Gly Ser Cys Phe Thr Ser		
115	120	125
aaa tcc acg cga gag tgg ctc gcg aga tgg ggg ata gca cac acc acc		432
Lys Ser Thr Arg Glu Trp Leu Ala Arg Trp Gly Ile Ala His Thr Thr		
130	135	140
ggg att ccg ggt aat tcc cag ggt caa gct atg gta gag cgg gcc aac		480
Gly Ile Pro Gly Asn Ser Gln Gly Gln Ala Met Val Glu Arg Ala Asn		
145	150	155
160		
cgg ctc ctg aaa gat agg atc cgt gtg ctt gcg gag ggg gac ggc ttt		528
Arg Leu Leu Lys Asp Arg Ile Arg Val Leu Ala Glu Gly Asp Gly Phe		
165	170	175
atg aaa aga atc ccc acc agc aaa cag ggg gaa cta tta gcc aag gca		576
Met Lys Arg Ile Pro Thr Ser Lys Gln Gly Glu Leu Leu Ala Lys Ala		
180	185	190
atg tat gcc ctc aat cac ttt gag cgt ggt gaa aac acg aaa aca ccg		624
Met Tyr Ala Leu Asn His Phe Glu Arg Gly Glu Asn Thr Lys Thr Pro		
195	200	205
ata caa aaa cac tgg aga cct acc gtt ctt aca gaa gga ccc ccg gtt		672
Ile Gln Lys His Trp Arg Pro Thr Val Leu Thr Glu Gly Pro Pro Val		
210	215	220
aaa ata cga ata gag aca ggg gag tgg gaa aaa gga tgg aac gtg ctg		720
Lys Ile Arg Ile Glu Thr Gly Glu Trp Glu Lys Gly Trp Asn Val Leu		
225	230	235
240		
gtc tgg gga cga ggt tat gcc gct gtg aaa aac agg gac act gat aag		768
Val Trp Gly Arg Gly Tyr Ala Ala Val Lys Asn Arg Asp Thr Asp Lys		
245	250	255
gtt att tgg gta ccc tct cga aaa gtt aaa ccg gac atc acc caa aag		816
Val Ile Trp Val Pro Ser Arg Lys Val Lys Pro Asp Ile Thr Gln Lys		
260	265	270
gat gag gtg act aag aaa gat gag gcg agc cct ctt ttt gca ggc att		864
Asp Glu Val Thr Lys Lys Asp Glu Ala Ser Pro Leu Phe Ala Gly Ile		
275	280	285
tct gac tgg ata ccc tgg gga gac aag caa gaa gga ctc caa gga gaa		912
Ser Asp Trp Ile Pro Trp Gly Asp Lys Gln Glu Gly Leu Gln Gly Glu		
290	295	300

acc gct agc aac aag caa gaa aga ccc gga gaa gac acc ctt gct gcc 960
Thr Ala Ser Asn Lys Gln Glu Arg Pro Gly Glu Asp Thr Leu Ala Ala
305 310 315 320

aac gag agt taa 972
Asn Glu Ser *

<210> 9
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed PCR primer including 5' region of GFP
gene and a part of NheI restriction enzyme site to
multiply GFP gene.

<400> 9
ctagcgctac cggtcgcccac c 21

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed PCR primer including antisense sequence
of GFP ORF to multiply a part of GFP gene.

<400> 10
gttgcgtcc tccttgaagt 20

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed PCR primer including U5 region LTR
sequence to
multiply a part of integrated plasmid vector.

<400> 11
tttgtgtgca cctgggttga t 21

<210> 12
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed PCR primer including 5' end of GFP ORF
sequence to multiply a part of GFP gene.

<400> 12
atggtgagca agggcgagga gctgttcacc ggggtg 36

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed PCR primer including a part of GFP ORF
sequence to multiply a part of GFP gene.

<400> 13
gtcgagctgg acggcgacgt 20